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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/776,910

DATE: 12/17/2001

TIME: 14:44:30

Input Set : N:\Crf3\RULE60\09776910.txt

Output Set: N:\CRF3\12172001\I776910.raw

3 <110> APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
5 <120> TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
7 <130> FILE REFERENCE: Attorney Docket No. 50179-051
9 <140> CURRENT APPLICATION NUMBER: 09/776,910
10 <141> CURRENT FILING DATE: 2001-02-06
12 <150> PRIOR APPLICATION NUMBER: 09/068,960
13 <151> PRIOR FILING DATE: 1998-06-20
15 <150> PRIOR APPLICATION NUMBER: PCT/AU96/00746
16 <151> PRIOR FILING DATE: 1996-11-22
18 <150> PRIOR APPLICATION NUMBER: AU 6751
19 <151> PRIOR FILING DATE: 1995-11-23
21 <160> NUMBER OF SEQ ID NOS: 43
23 <170> SOFTWARE: PatentIn Ver 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1713
27 <212> TYPE: DNA
28 <213> ORGANISM: Lucilia cuprina
30 <400> SEQUENCE: 1

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33 aaagtgaag gcgttaaacg tttaactgtg tacgatgatt cctactacag ttttgaggg 180
34 ataccgtacg cccaaccgcc agtgggtgag ctgagattta aagcacccca gcgaccaaca 240
35 ccttgggatg gtgtgcgtga ttgttgcaat cataaagata agtcagtgc agttgatttt 300
36 ataacgggca aagtgtgtgg ctacagaggat tgtctatacc taagtgtcta tacgaataat 360
37 ctaaatcccg aaactaaacg tcccgtttta gtatacatat atggtggtgg ttttattatc 420
38 ggtgaaaatc atcgtgatat gtatggctct gattatttca ttaaaaagga tgtggtgttg 480
39 attaacatac aatatcgttt gggagctcta ggttttctaa gtttaaatc agaagacctt 540
40 aatgtgcccg gtaatgcccg ccttaaagat caagtcattg ccttgcttg gattaaaaat 600
41 aattgcgcca actttggttg caatcccgat aatattacag tctttggtga aagtgccggt 660
42 gctgctcta cccactacat gatgttaacc gaacaaactc gcggtctttt ccatcgttgt 720
43 atactaatgt cgggtaatgc tatttgtcca ttggctaata cccaatgtca acatcgtgcc 780
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45 tttcttatga aagccaagcc acaggattta ataaaacttg aggaaaaagt ttaactcta 900
46 gaagagcgta caaataaggt catgtttcct tttggtccca ctgttgagcc atatcagacc 960
47 gctgattgtg tcttacccaa acatcctcgg gaaatggtta aaactgcttg gggtaattcg 1020
48 ataccacta tgatgggtaa cacttcatat gagggctctat ttttcacttc aattcttaag 1080
49 caaatgccta tgcctgttaa ggaattggaa acttgtgtca atttgtgcc aagtgaattg 1140
50 gctgatgttg aacgcaccgc cccagagacc ttggaaatgg gtgctaaaat taaaaaggct 1200
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55 aatcaattgg ccaaacgtat gcctaaagaa tcgctgtaat acaaaacaat tgaacgtatg 1500
56 actggtatat ggatacaatt tgccaccact ggtaatcctt atagcaatga aattgaagg 1560
57 atggaaaatg tttcctggga tccaattaag aaatccgatg aagtatacaa gtgtttgaat 1620
58 attagtgatg aattgaaaat gattgatgtg cctgaaatgg ataagattaa acaatgggag 1680
59 tcgatgtttg aaaaacatag agatttttt tag 1713

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61 <210> SEQ ID NO: 2
62 <211> LENGTH: 570
63 <212> TYPE: PRI
64 <213> ORGANISM: Lucilia cuprina
66 <400> SEQUENCE: 2
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70 Cys Ile Glu Asn Lys Phe Leu Asn Tyr Arg Leu Thr Thr Asn Glu Thr
71               20               25               30
73 Val Val Ala Glu Thr Glu Tyr Gly Lys Val Lys Gly Val Lys Arg Leu
74               35               40               45
76 Thr Val Tyr Asp Asp Ser Tyr Tyr Ser Phe Glu Gly Ile Pro Tyr Ala
77   50               55               60
79 Gln Pro Pro Val Gly Glu Leu Arg Phe Lys Ala Pro Gln Arg Pro Thr
80   65               70               75               80
82 Pro Trp Asp Gly Val Arg Asp Cys Cys Asn His Lys Asp Lys Ser Val
83               85               90               95
85 Gln Val Asp Phe Ile Thr Gly Lys Val Cys Gly Ser Glu Asp Cys Leu
86   100              105              110
88 Tyr Leu Ser Val Tyr Thr Asn Asn Leu Asn Pro Glu Thr Lys Arg Pro
89   115              120              125
91 Val Leu Val Tyr Ile His Gly Gly Gly Phe Ile Ile Gly Glu Asn His
92   130              135              140
94 Arg Asp Met Tyr Gly Pro Asp Tyr Phe Ile Lys Lys Asp Val Val Leu
95  145              150              155              160
97 Ile Asn Ile Gln Tyr Arg Leu Gly Ala Leu Gly Phe Leu Ser Leu Asn
98   165              170              175
100 Ser Glu Asp Leu Asn Val Pro Gly Asn Ala Gly Leu Lys Asp Gln Val
101   180              185              190
103 Met Ala Leu Arg Trp Ile Lys Asn Cys Ala Asn Phe Gly Gly Asn
104   195              200              205
106 Pro Asp Asn Ile Thr Val Phe Gly Glu Ser Ala Gly Ala Ala Ser Thr
107   210              215              220
109 His Tyr Met Met Leu Thr Glu Gln Thr Arg Gly Leu Phe His Arg Gly
110  225              230              235              240
112 Ile Leu Met Ser Gly Asn Ala Ile Cys Pro Leu Ala Asn Thr Gln Cys
113   245              250              255
115 Gln His Arg Ala Phe Thr Leu Ala Lys Leu Ala Gly Tyr Lys Gly Glu
116   260              265              270
118 Asp Asn Asp Lys Asp Val Leu Glu Phe Leu Met Lys Ala Lys Pro Gln
119   275              280              285
121 Asp Leu Ile Lys Leu Glu Glu Lys Val Leu Thr Leu Glu Glu Arg Thr
122   290              295              300
124 Asn Lys Val Met Phe Pro Phe Gly Pro Thr Val Glu Pro Tyr Gln Thr
125  305              310              315              320
127 Ala Asp Cys Val Leu Pro Lys His Pro Arg Glu Met Val Lys Thr Ala
128   325              330              335
130 Trp Gly Asn Ser Ile Pro Thr Met Met Gly Asn Thr Ser Tyr Glu Gly
131   340              345              350

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133 Leu Phe Phe Thr Ser Ile Leu Lys Gln Met Pro Met Leu Val Lys Glu
134          355          360          365
136 Leu Glu Thr Cys Val Asn Phe Val Pro Ser Glu Leu Ala Asp Ala Glu
137          370          375          380
139 Arg Thr Ala Pro Glu Thr Leu Glu Met Gly Ala Lys Ile Lys Lys Ala
140 385          390          395          400
142 His Val Thr Gly Glu Thr Pro Thr Ala Asp Asn Phe Met Asp Leu Cys
143          405          410          415
145 Ser His Ile Tyr Phe Trp Phe Pro Met His Arg Leu Leu Gln Leu Arg
146          420          425          430
148 Phe Asn His Thr Ser Gly Thr Pro Val Tyr Leu Tyr Arg Phe Asp Phe
149          435          440          445
151 Asp Ser Glu Asp Leu Ile Asn Pro Tyr Arg Ile Met Arg Ser Gly Arg
152          450          455          460
154 Gly Val Lys Gly Val Ser His Ala Asp Glu Leu Thr Tyr Phe Phe Trp
155 465          470          475          480
157 Asn Gln Leu Ala Lys Arg Met Pro Lys Glu Ser Arg Glu Tyr Lys Thr
158          485          490          495
160 Ile Glu Arg Met Thr Gly Ile Trp Ile Gln Phe Ala Thr Thr Gly Asn
161          500          505          510
163 Pro Tyr Ser Asn Glu Ile Glu Gly Met Glu Asn Val Ser Trp Asp Pro
164          515          520          525
166 Ile Lys Lys Ser Asp Glu Val Tyr Lys Cys Leu Asn Ile Ser Asp Glu
167          530          535          540
169 Leu Lys Met Ile Asp Val Pro Glu Met Asp Lys Ile Lys Gln Trp Glu
170 545          550          555          560
172 Ser Met Phe Glu Lys His Arg Asp Leu Phe
173          565          570
176 <210> SEQ ID NO: 3
177 <211> LENGTH: 1713
178 <212> TYPE: DNA
179 <213> ORGANISM: Lucilia cuprina
181 <400> SEQUENCE: 3
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184 aaagtgaag gcgtaaacg tttaactgtg tacgatgatt cctactacag ttttgagggt 180
185 ataccgtacg cccaaccgcc agtgggtgag ctgagattta aagcacccca gcgaccaaca 240
186 ccctgggatg gtgtgcgcga ttgttgcaat cataaagata agtcagtgca agttgatttt 300
187 ataacgggca aagtgtgtgg ctacaggat tgtctatacc taagtgtcta tacgaataat 360
188 ctaaatcccg aaactaaacg tcccgtttta gtatacatat atggtggtgg ttttattatc 420
189 ggtgaaaatc atcgtgatat gtatggtcct gattatttca ttaaaaagga tgtgggtgtg 480
190 altaacatac aatatcgttt gggagctcta ggttttctaa gtttaaatc agaagacctt 540
191 aatgtgcccg gtaatgccgg ccttaaagat caagtcattg ccttgcggtg gattaaaaat 600
192 aattgcgcca actttggtgg caatcccgat aatattacag tctttggtga aagtgccggg 660
193 gctgcctcta cccactacat gatgttaacc gaacaaactc gcggtctttt ccacgtggtg 720
194 atactaatgt cgggtaattgc tatttgcca ttggctaata ccaatgtca acatcggtgc 780
195 ttcaccttag ccaaattggc cggctataag ggtgaggata atgataagga tgttttgga 840
196 tttcttatga aagccaagcc acaggattta ataaaacttg aggaaaaagt tttaactcta 900
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198 gctgattgtg tcttacccaa acatcctcgg gaaatgggta aaactgcttg gggtaattcg 1020
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200 caaatgccta tgcttggttaa ggaattggaa acttggtgca attttgtgcc aagtgaattg 1140
201 gctgatgctg aacgcaccgc ccagagagcc ttggaaatgg gtgctaaaat taaaaaggct 1200
202 catgttacag gagaaacacc aacagctgat aattttatgg atctttgctc tcacatctat 1260
203 ttctggttcc ccattgcacg ttgttgcaaa ttacgtttca atcacacctc cggtaacacc 1320
204 gtctacttgt atcgtcttga cttegatctg gaagatctta tcaatcccta tcgtattatg 1380
205 cgtagtggac gtggtgttaa ggggtgttagt catgctgatg aattaacctt tttcttcttg 1440
206 aatcaattgg ccaaacgtat gcctaaagaa tcgcgtgaat acaaaacaat tgaacgtatg 1500
207 actggtatat ggatacaatt tgcaccact ggtaatcctt atagcaatga aattgaagg 1560
208 atggaaaatg tttctgga tccaattaag aaatccgatg aagtatacaa gtgtttgaat 1620
209 attagtgatg aattgaaaat gattgatgtg cctgaaatgg ataagattaa acaatgggag 1680
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212 <210> SEQ ID NO: 4

213 <211> LENGTH: 570

214 <212> TYPE: PRT

215 <213> ORGANISM: *Lucilia cuprina*

217 <400> SEQUENCE: 4

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222 20 25 30
224 Val Val Ala Glu Thr Glu Tyr Gly Lys Val Lys Gly Val Lys Arg Leu
225 35 40 45
227 Thr Val Tyr Asp Asp Ser Tyr Tyr Ser Phe Glu Gly Ile Pro Tyr Ala
228 50 55 60
230 Gln Pro Pro Val Gly Glu Leu Arg Phe Lys Ala Pro Gln Arg Pro Thr
231 65 70 75 80
233 Pro Trp Asp Gly Val Arg Asp Cys Cys Asn His Lys Asp Lys Ser Val
234 85 90 95
236 Gln Val Asp Phe Ile Thr Gly Lys Val Cys Gly Ser Glu Asp Cys Leu
237 100 105 110
239 Tyr Leu Ser Val Tyr Thr Asn Asn Leu Asn Pro Glu Thr Lys Arg Pro
240 115 120 125
242 Val Leu Val Tyr Ile His Gly Gly Gly Phe Ile Ile Gly Glu Asn His
243 130 135 140
245 Arg Asp Met Tyr Gly Pro Asp Tyr Phe Ile Lys Lys Asp Val Val Leu
246 145 150 155 160
248 Ile Asn Ile Gln Tyr Arg Leu Gly Ala Leu Gly Phe Leu Ser Leu Asn
249 165 170 175
251 Ser Glu Asp Leu Asn Val Pro Gly Asn Ala Gly Leu Lys Asp Gln Val
252 180 185 190
254 Met Ala Leu Arg Trp Ile Lys Asn Asn Cys Ala Asn Phe Gly Gly Asn
255 195 200 205
257 Pro Asp Asn Ile Thr Val Phe Gly Glu Ser Ala Gly Ala Ala Ser Thr
258 210 215 220
260 His Tyr Met Met Leu Thr Glu Gln Thr Arg Gly Leu Phe His Arg Gly
261 225 230 235 240
263 Ile Leu Met Ser Gly Asn Ala Ile Cys Pro Leu Ala Asn Thr Gln Cys

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264          245          250          255
266 Gln His Arg Ala Phe Thr Leu Ala Lys Leu Ala Gly Tyr Lys Gly Glu
267          260          265          270
269 Asp Asn Asp Lys Asp Val Leu Glu Phe Leu Met Lys Ala Lys Pro Gln
270          275          280          285
272 Asp Leu Ile Lys Leu Glu Glu Lys Val Leu Thr Leu Glu Glu Arg Thr
273          290          295          300
275 Asn Lys Val Met Phe Pro Phe Gly Pro Thr Val Glu Pro Tyr Gln Thr
276 305          310          315          320
278 Ala Asp Cys Val Leu Pro Lys His Pro Arg Glu Met Val Lys Thr Ala
279          325          330          335
281 Trp Gly Asn Ser Ile Pro Thr Met Met Gly Asn Thr Ser Tyr Glu Gly
282          340          345          350
284 Leu Phe Phe Thr Ser Ile Leu Lys Gln Met Pro Met Leu Val Lys Glu
285          355          360          365
287 Leu Glu Thr Cys Val Asn Phe Val Pro Ser Glu Leu Ala Asp Ala Glu
288          370          375          380
290 Arg Thr Ala Pro Glu Thr Leu Glu Met Gly Ala Lys Ile Lys Lys Ala
291 385          390          395          400
293 His Val Thr Gly Glu Thr Pro Thr Ala Asp Asn Phe Met Asp Leu Cys
294          405          410          415
296 Ser His Ile Tyr Phe Trp Phe Pro Met His Arg Leu Leu Gln Leu Arg
297          420          425          430
299 Phe Asn His Thr Ser Gly Thr Pro Val Tyr Leu Tyr Arg Phe Asp Phe
300          435          440          445
302 Asp Ser Glu Asp Leu Ile Asn Pro Tyr Arg Ile Met Arg Ser Gly Arg
303          450          455          460
305 Gly Val Lys Gly Val Ser His Ala Asp Glu Leu Thr Tyr Phe Phe Trp
306 465          470          475          480
308 Asn Gln Leu Ala Lys Arg Met Pro Lys Glu Ser Arg Glu Tyr Lys Thr
309          485          490          495
311 Ile Glu Arg Met Thr Gly Ile Trp Ile Gln Phe Ala Thr Thr Gly Asn
312          500          505          510
314 Pro Tyr Ser Asn Glu Ile Glu Gly Met Glu Asn Val Ser Trp Asp Pro
315          515          520          525
317 Ile Lys Lys Ser Asp Glu Val Tyr Lys Cys Leu Asn Ile Ser Asp Glu
318          530          535          540
320 Leu Lys Met Ile Asp Val Pro Glu Met Asp Lys Ile Lys Gln Trp Glu
321 545          550          555          560
323 Ser Met Phe Glu Lys His Arg Asp Leu Phe
324          565          570
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328 <211> LENGTH: 1713
329 <212> TYPE: DNA
330 <213> ORGANISM: Lucilia cuprina
332 <400> SEQUENCE: 5
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335 aaagtgaaag gcgttaaacg tttaactgtg tacgatgatt cctactacag ttttgagggt 180

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09776910.txt

Output Set: N:\CRF3\12172001\I776910.raw

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